

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

```
Run on:      October 21, 2005, 15:14:21 ; Search time 19.3333 Seconds
            (without alignments)
            79.628 Million cell updates/sec
```

Title: US-10-001-938-19
Perfect score: 84
Sequence: 1 EAYEVLSDKHKREIYD 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 0

```
Minimum DB seq length: 16
Maximum DB seq length: 16
```

Post-processing:	Minimum Match	100%
	Maximum Match	100%
	Listing first	45 s

```
Database :      PIR_79:*
1:  pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	100	100	100	100	100	100
2	95	95	95	95	95	95
3	90	90	90	90	90	90
4	85	85	85	85	85	85
5	80	80	80	80	80	80
6	75	75	75	75	75	75
7	70	70	70	70	70	70
8	65	65	65	65	65	65
9	60	60	60	60	60	60
10	55	55	55	55	55	55
11	50	50	50	50	50	50
12	45	45	45	45	45	45
13	40	40	40	40	40	40
14	35	35	35	35	35	35
15	30	30	30	30	30	30
16	25	25	25	25	25	25
17	20	20	20	20	20	20
18	15	15	15	15	15	15
19	10	10	10	10	10	10
20	5	5	5	5	5	5

No matches found

Search completed: October 21, 2005, 15:36:11
Job time : 19.3333 secs

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OM protein - protein search, using sw model

```
Run on:      October 21, 2005, 15:14:21 ; Search time 91.6667 Seconds
            (without alignments)
            89.381 Million cell updates/sec
```

Title: US-10-001-938-19
Perfect score: 84
Sequence: 1 EAYEVLSDKHKREIYD 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 0

```
Minimum DB seq length: 16
Maximum DB seq length: 16
```

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

```
Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	100	100	100	100	100	100
2	95	95	95	95	95	95
3	90	90	90	90	90	90
4	85	85	85	85	85	85
5	80	80	80	80	80	80
6	75	75	75	75	75	75
7	70	70	70	70	70	70
8	65	65	65	65	65	65
9	60	60	60	60	60	60
10	55	55	55	55	55	55
11	50	50	50	50	50	50
12	45	45	45	45	45	45
13	40	40	40	40	40	40
14	35	35	35	35	35	35
15	30	30	30	30	30	30
16	25	25	25	25	25	25
17	20	20	20	20	20	20
18	15	15	15	15	15	15
19	10	10	10	10	10	10
20	5	5	5	5	5	5

No matches found

Search completed: October 21, 2005, 15:35:11
Job time : 91.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2005, 15:14:21 ; Search time 25.6667 Seconds
(without alignments)
46.534 Million cell updates/sec

Title: US-10-001-938-19
Perfect score: 84
Sequence: 1 EAYEVLSDKHKEIYD 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

No matches found

Search completed: October 21, 2005, 15:15:49
Job time : 25.6667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 15:30:41 ; Search time 94 Seconds
 (without alignments)
 71.062 Million cell updates/sec

Title: US-10-001-938-19
Perfect score: 84
Sequence: 1 EAYEVLSDKHKREIYD 16

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 100%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				
Result	Query			
No.	Score	Match	Length	ID Description

1	84	100.0	16	14 US-10-001-938-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-001-938-19
; Sequence 19, Application US/10001938
; Publication No. US20030031679A1
; GENERAL INFORMATION:

; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: CARSON, Dennis
; APPLICANT: PRAKEN, Berent
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: UCSD1360-1
; CURRENT APPLICATION NUMBER: US/10/001,938
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/245,181
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-001-938-19

Query Match 100.0%; Score 84; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAYEVLSDKHKREIYD 16
 | | | | | | | | | | | | | | | |
Db 1 EAYEVLSDKHKREIYD 16

Search completed: October 21, 2005, 15:48:52
Job time : 94 secs

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OM protein - protein search, using sw model

Run on:October 21, 2005, 15:14:22 ; Search time 100.667 Seconds
(without alignments)
61.472 Million cell updates/sec

Title:US-10-001-938-3
Perfect score:86
Sequence:1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:2

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match %	Length DB	ID Description
1	86	100.0	16	5 AAU98852 Aau98852 E.Coli DN
2	86	100.0	16	6 ABR55126 ABR55126 E. coli d

ALIGNMENTS	
RESULT 1	
AAU98852	
ID	AAU98852 standard; peptide; 16 AA.
XX	
AC	AAU98852;
XX	
DT	22-AUG-2002 (first entry)
XX	
DE	E.Coli DNAJ 61 immunogenic peptide.
XX	
KW	Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory;
KW	cytostatic; antiinflammatory; antibacterial; antiarthritic;
KW	autoimmune disease; arthritis; articular juvenile idiopathic arthritis;
KW	infectious disease; inflammatory bowel disease; cancer;
KW	mucosal tolerisation; DNA vaccination; anergy induction.
XX	
OS	Escherichia coli.
XX	

PN	WO200236611-A2.				
XX					
PD	10-MAY-2002.				
XX					
PF	31-OCT-2001; 2001WO-US045344.				
XX					
PR	01-NOV-2000; 2000US-0245181P.				
XX					
PA	(REGC) UNIV CALIFORNIA.				
PA	(MART/) MARTINI A.				
XX					
PI	Martini A, Albani S, Carson DA, Prakken BJ;				
XX					
DR	WPI; 2002-489999/52.				
XX					
PPT	New immunomodulatory peptides from heat shock proteins, useful for treating immunological disorder in subjects such as humans, e.g. autoimmune disease (e.g. arthritis), infectious disease, inflammatory bowel disease or cancer.				
PPT					
XX					
PS	Claim 4; Page 55; 84pp; English.				
XX					
CC	This invention relates to the use of a peptide, which is an immunogenic portion derived from a dnaJ heat shock protein (hsp) in modulating an immune response in a subject. The peptides of the invention may have immunomodulatory, cytostatic, antiinflammatory, antibacterial or antiarthritic properties and can stimulate expression of interleukins, tumour necrosis factor and transforming growth factor beta. The immunogenic peptide is useful for modulating (i.e. augmenting/inducing or reducing/inhibiting) an immune response in a subject having an immunological disorder (e.g. autoimmune disease such as arthritis or articular juvenile idiopathic arthritis), an infectious disease, an inflammatory bowel disease or cancer. The immunogenic peptide of the invention is also useful for modulating immunoeffector cell responsiveness in a subject. The immunogenic peptide is particularly useful for treating the above-mentioned diseases in mammals, e.g. cat, dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In general, the peptide is useful in methods involving mucosal tolerisation, DNA vaccination, anergy induction or active immunisation. The present sequence represents an E. coli DNAJ immunogenic peptide of the invention				
XX					
SQ	Sequence 16 AA;				
	Query Match	100.0%;	Score 86;	DB 5;	Length 16;
	Best Local Similarity	100.0%;	Pred. No. 4.7e-08;		
	Matches	16; Conservative	0; Mismatches	0; Indels	0; Gaps
					0;
QY	1	QKRAAYDQYGHAAFEQ	16		
Db	1	QKRAAYDQYGHAAFEQ	16		
RESULT 2					
ABR55126					
ID	ABR55126	standard; peptide;	16 AA.		
XX					
AC	ABR55126;				
XX					
DT	03-JUL-2003	(first entry)			
XX					
DE	E. coli dnaJ61	antigen-specific epitope peptide.			
XX					
KW	Antigen-specific epitope;	immune response; T cell; cytokine;			
KW	antiarthritic;	antidiabetic; neuroprotective; anti-inflammatory;			
KW	cytostatic; antithyroid;	anti-asthmatic; immunosuppressive;			
KW	antipsoriatic;	anti-ulcer; antianaemic; cardiant; respiratory;			
KW	antiallergic;	dermatological; antipsoriatic.			
XX					
OS	Escherichia coli.				
XX					
PN	WO2003026579-A2.				
XX					
PD	03-APR-2003.				

XX 25-SEP-2002; 2002WO-US030578.
PF XX
XX 25-SEP-2001; 2001US-0325499P.
PR 11-DEC-2001; 2001US-0339284P.
PR XX
XX (REGC) UNIV CALIFORNIA.
PA XX
XX Albani S, Martins A;
PI XX
XX WPI; 2003-430097/40.
DR XX
XX Modulating an immune response in a subject having an immune-related
PT disorder, e.g. arthritis by administering an antigen-specific epitope and
PT a cytokine or an agent that effects cytokine activity or expression.
PT XX
PS Disclosure; Page 9; 41pp; English.
PS XX
CC The invention relates to a novel method for modulating an immune response
CC in a subject having an immune-related disorder. The method comprises: (a)
CC administering an antigen-specific epitope, where administration provides
CC epitope-specific T cell immune modulation; and (b) administering a
CC cytokine, an agent that effects cytokine activity or expression, or an
CC anticytokine therapy. The method of the invention has antiarthritic,
CC antidiabetic, neuroprotective, anti-inflammatory, cytostatic,
CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-
CC ulcer, antianaemic, cardiant, respiratory general, antiallergic,
CC dermatological, and antipsoriatic activity. The method is useful for
CC modulating an immune response in a subject having an immune-related
CC disorder. The present sequence is used in the exemplification of the
CC invention
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 86; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFEQ 16

Search completed: October 21, 2005, 15:41:20
Job time : 101.667 secs

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OM protein - protein search, using sw model

Run on: October 21, 2005, 15:14:21 ; Search time 19.3333 Seconds
 (without alignments)
 79.628 Million cell updates/sec

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 100%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_79:*
 1: pirl:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description

No matches found

Search completed: October 21, 2005, 15:36:11
Job time : 19.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2005, 15:14:21 ; Search time 91.6667 Seconds
 (without alignments)
 89.381 Million cell updates/sec

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 100%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

§			
Result	Query		
No.	Score	Match Length DB ID	Description

No matches found

Search completed: October 21, 2005, 15:35:10
Job time : 99.6667 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

```
Run on:      October 21, 2005, 15:14:21 ; Search time 25.6667 Seconds
            (without alignments)
            46.534 Million cell updates/sec
```

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 0

```
Minimum DB seq length: 16
Maximum DB seq length: 16
```

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

```
Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCtUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
---------------	-------	----------------	--------	----	----	-------------

No matches found

Search completed: October 21, 2005, 15:15:49
Job time : 25.6667 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 15:30:41 ; Search time 94 Seconds
(without alignments)
71.062 Million cell updates/sec

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6:	/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9:	/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10:	/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11:	/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16:	/cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17:	/cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
18:	/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
19:	/cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
20:	/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
21:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	16	14 US-10-001-938-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-001-938-3
; Sequence 3, Application US/10001938
; Publication No. US20030031679A1
; GENERAL INFORMATION:

; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: CARSON, Dennis
; APPLICANT: PRAKKEN, Berent
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: UCSD1360-1
; CURRENT APPLICATION NUMBER: US/10/001,938
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/245,181
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-001-938-3

Query Match 100.0%; Score 86; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFEQ 16

Search completed: October 21, 2005, 15:48:52
Job time : 94 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2005, 15:14:22 ; Search time 100.667 Seconds
(without alignments)
61.472 Million cell updates/sec

Title: US-10-001-938-19
Perfect score: 84
Sequence: 1 EAYEVLSDKHKREIYD 16
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 16
Maximum DB seq length: 16

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	84	100.0	16	2	AAW59453	Aaw59453 Human HSJ
2	84	100.0	16	5	AAU98868	Aau98868 Human HSJ
3	84	100.0	16	6	ABR55150	Abr55150 Human 51(

ALIGNMENTS

RESULT 1	
AAW59453	
ID	AAW59453 standard; peptide; 16 AA.
XX	
AC	AAW59453;
XX	
DT	28-AUG-1998 (first entry)
XX	
DE	Human HSJ-1a protein DnaJ domain antigenic peptide fragment.
XX	
KW	Tumour-associated antigen; h-Tid; polyclonal antibody; human; HSJ-1a;
KW	DnaJ domain; detection; colonic; endometrial; adenocarcinoma; mammary;
KW	pulmonary; cervical; carcinoma.
XX	
OS	Homo sapiens.
XX	
PN	DE19702065-C1.

XX	20-MAY-1998.	
PD		
XX	XX	
PF	22-JAN-1997; 97DE-01002065.	
XX	XX	
PR	22-JAN-1997; 97DE-01002065.	
XX	XX	
PA	(KURZ/) KURZIK-DUMKE U.	
XX	XX	
PI	Kurzik-Dumke U;	
XX	XX	
DR	WPI; 1998-262548/24.	
XX	XX	
PT	Polyclonal antibody for detection of tumour-associated antigen hTid -	
PT	useful in assays for diagnosis of cancer.	
XX	XX	
PS	Claim 1; Col 5; 4pp; German.	
XX	XX	
CC	This peptide fragment is derived from the human HSJ-1a protein DnaJ domain and is used to raise polyclonal antibodies for detection of the tumour-associated antigen hTid. The antibody is used in an ELISA assay for hTid in a sample of body fluid or tissue extract, especially for detecting pathologically altered hTid expression in cells. The detection method involves immobilising the sample on a solid support, contacting the sample with the antibody, adding an antibody that specifically binds to the first antibody and is labelled with an enzyme that catalyses the conversion of a colourless substrate to a coloured product, adding the colourless substrate, and measuring the coloured product. The assay provides a simple and unequivocal means of detecting the human hTid protein, expression of which is characteristic of colonic and endometrial adenocarcinoma and mammary, pulmonary and cervical carcinoma	
XX	XX	
SQ	Sequence 16 AA;	
Query Match 100.0%; Score 84; DB 2; Length 16;		
Best Local Similarity 100.0%; Pred. No. 9.2e-07;		
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 EAYEVLSDKHKREIYD 16	
Db	1 EAYEVLSDKHKREIYD 16	
RESULT 2		
AAU98868		
ID	AAU98868	standard; peptide; 16 AA.
XX	XX	
AC	AAU98868;	
XX	XX	
DT	22-AUG-2002	(first entry)
XX	XX	
DE	Human HSJI	immunogenic peptide #5.
XX	XX	
KW	Immunogenic peptide; heat shock protein; HSP; DnaJ; immunomodulatory; cytostatic; antiinflammatory; antibacterial; antiarthritic; human;	
KW	autoimmune disease; arthritis; articular juvenile idiopathic arthritis;	
KW	infectious disease; inflammatory bowel disease; cancer; HSJI;	
KW	mucosal tolerisation; DNA vaccination; anergy induction.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
PN	WO200236611-A2.	
XX	XX	
PD	10-MAY-2002.	
XX	XX	
PF	31-OCT-2001; 2001WO-US045344.	
XX	XX	
PR	01-NOV-2000; 2000US-0245181P.	
XX	XX	
PA	(REGC) UNIV CALIFORNIA.	
PA	(MART/) MARTINI A.	
XX	XX	
PI	Martini A, Albani S, Carson DA, Prakken BJ;	

XX WPI; 2002-489999/52.

XX New immunomodulatory peptides from heat shock proteins, useful for

PT treating immunological disorder in subjects such as humans, e.g.

PT autoimmune disease (e.g. arthritis), infectious disease, inflammatory

PT bowel disease or cancer.

XX Claim 12; Page 57; 84pp; English.

XX This invention relates to the use of a peptide, which is an immunogenic

CC portion derived from a dnaJ heat shock protein (hsp) in modulating an

CC immune response in a subject. The peptides of the invention may have

CC immunomodulatory, cytotstatic, antiinflammatory, antibacterial or

CC antiarthritic properties and can stimulate expression of interleukins,

CC tumour necrosis factor and transforming growth factor beta. The

CC immunogenic peptide is useful for modulating (i.e. augmenting/inducing or

CC reducing/inhibiting) an immune response in a subject having an

CC immunological disorder (e.g. autoimmune disease such as arthritis or

CC articular juvenile idiopathic arthritis), an infectious disease, an

CC inflammatory bowel disease or cancer. The immunogenic peptide of the

CC invention is also useful for modulating immunoeffector cell

CC responsiveness in a subject. The immunogenic peptide is particularly

CC useful for treating the above-mentioned diseases in mammals, e.g. cat,

CC dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In

CC general, the peptide is useful in methods involving mucosal tolerisation,

CC DNA vaccination, anergy induction or active immunisation. The present

CC sequence represents a human heat shock protein immunogenic peptide of the

CC invention

XX

SQ Sequence 16 AA;

Query Match 100.0%; Score 84; DB 5; Length 16;

Best Local Similarity 100.0%; Pred. No. 9.2e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAYEVLSDKHKREIYD 16

Db 1 EAYEVLSDKHKREIYD 16

RESULT 3

ABR55150

ID ABR55150 standard; peptide; 16 AA.

XX

AC ABR55150;

XX

DT 03-JUL-2003 (first entry)

XX

DE Human 51(HSJ1) antigen-specific epitope peptide.

XX

KW Antigen-specific epitope; immune response; T cell; cytokine;

KW antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;

KW cytotstatic; antithyroid; anti-asthmatic; immunosuppressive;

KW antipsoriatic; anti-ulcer; antianaemic; cardiant; respiratory;

KW antiallergic; dermatological; antipsoriatic; human.

XX

OS Homo sapiens.

XX

PN WO2003026579-A2.

XX

PD 03-APR-2003.

XX

PF 25-SEP-2002; 2002WO-US030578.

XX

PR 25-SEP-2001; 2001US-0325499P.

PR 11-DEC-2001; 2001US-0339284P.

XX

XX (REGC) UNIV CALIFORNIA.

FA

XX Albani S, Martins A;

PI

XX WPI; 2003-430097/40.

DR

XX

PT Modulating an immune response in a subject having an immune-related

PT disorder, e.g. arthritis by administering an antigen-specific epitope and

PT a cytokine or an agent that effects cytokine activity or expression.

XX

PS Disclosure; Page 9; 4lpp; English.

XX

CC The invention relates to a novel method for modulating an immune response

CC in a subject having an immune-related disorder. The method comprises: (a)

CC administering an antigen-specific epitope, where administration provides

CC epitope-specific T cell immune modulation; and (b) administering a

CC cytokine, an agent that effects cytokine activity or expression, or an

CC anticytokine therapy. The method of the invention has antiarthritic,

CC antidiabetic, neuroprotective, anti-inflammatory, cytotstatic, anti-

CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-

CC ulcer, antianaemic, cardiant, respiratory general, antiallergic,

CC dermatological, and antipsoriatic activity. The method is useful for

CC modulating an immune response in a subject having an immune-related

CC disorder. The present sequence is used in the exemplification of the

CC invention

XX

SQ Sequence 16 AA;

Query Match 100.0%; Score 84; DB 6; Length 16;

Best Local Similarity 100.0%; Pred. No. 9.2e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAYEVLSDKHKREIYD 16

Db 1 EAYEVLSDKHKREIYD 16

Search completed: October 21, 2005, 15:41:21

Job time : 101.667 secs